

In the Claims:

Please amend the claims as follows:

Claims 1-7. (Canceled)

8. (New) A method for designing an antisense oligonucleotide sequence for a target mRNA or its precursor comprising the steps of:
- (a) selecting all pairs of sequences on the target mRNA or its precursor complementary to each other and separated by at least three nucleotides, without independently selecting pairs which are shorter than the selected sequences;
 - (b) assigning a numerical value to each pair that reflects the possibility of forming a complementary double-stranded region between said pair of sequences based upon the distance between said pair of sequences and the bond energy ΔG for said pair of sequences, wherein a lower numerical value indicates a lower possibility, and wherein the numerical value increases with an increase in said bond energy and the value decreases with an increase in the distance between said paired sequences;
 - (c) assigning the numerical value obtained in step (b) to each nucleotide of the paired sequences;
 - (d) summing the numerical values, which are assigned in step (c) for all pairs of sequences selected in step (a), for each nucleotide in the target mRNA or its precursor;
 - (e) selecting one or more regions which consist of at least 6 contiguous nucleotides and have a low summed value relative to another region; and
 - (f) designing an antisense oligonucleotide complementary to said region selected in step (e).
9. (New) The method of claim 8, wherein said bond energy for forming the complementary double-stranded region is determined by the nearest neighbor model.

10. (New) The method of claim 8, wherein said step (a) is conducted by the steps:
 - (a) selecting a first sequence consisting of 2 or more nucleotides from the target mRNA or its precursor;
 - (b) selecting a second sequence that is complementary to the first sequence and is separated by at least three nucleotides from the first sequence;
 - (c) examining whether the first and second sequences can be extended to include neighboring nucleotides by checking complementarity between corresponding neighboring nucleotides of each of the first and second sequences;
 - (d) extending each of the first and second sequences by one nucleotide when complementarity is found in step (c);
 - (e) repeating steps (c) and (d) in both directions of the first and second sequences until complementarity is not found;
 - (f) determining the sequences thereby selected;
 - (g) repeating steps (b) through (f) starting at a different region from that already selected in step (b) until all complementary second sequences for said first sequence have been selected; and
 - (h) repeating steps (a) through (g) for all possible first sequences on the target mRNA or its precursor without selecting the same pair more than once.
11. (New) The method of claim 8, wherein said numerical value is expressed as $((L+1)/r)^F \cdot \exp(|\Delta G|/RT)$, wherein ΔG is the bond energy for forming a complementary double-stranded region, R is the gas constant, T is the absolute temperature, L is an integer from 3 to 10, r is one plus the number of nucleic acid bases between said first target region and said complementary region, with the provision that $r > L+1$, and F is a positive number not greater than 6.
12. (New) The method of claim 11, wherein $|\Delta G|$ is determined by the nearest neighbor model.

13. (New) The method of claim 11, wherein L is 4 to 6.
14. (New) The method of claim 11, wherein L is 4.
15. (New) The method of claim 11, wherein F is 6.
16. (New) The method of claim 11, wherein L is 4 to 6, and $|\Delta G|$ is determined by the nearest neighbor model.
17. (New) The method of claim 11, wherein L is 4, and $|\Delta G|$ is determined by the nearest neighbor model.
18. (New) A method for designing an antisense oligonucleotide sequence for a target mRNA or its precursor comprising the steps of:
 - (a) selecting a first sequence consisting of 2 or more nucleotides in the target mRNA or its precursor;
 - (b) selecting a second sequence that is complementary to the first sequence that is separated by at least three nucleotides from the first sequence;
 - (c) examining whether the first and second sequences can be extended to include neighboring nucleotides by checking complementarity between corresponding neighboring nucleotides of each of the first and second sequences;
 - (d) extending each of the first and second sequences by one nucleotide when complementarity is found in step (c);
 - (e) repeating steps (c) and (d) in both directions of the first and second sequences until complementarity is not found;
 - (f) determining the sequences thereby selected;
 - (g) assigning a numerical value to said sequences that reflects the possibility of forming a complementary double-stranded region between said sequences based upon the distance between said sequences and the bond energy ΔG for said

- sequences, wherein a lower numerical value indicates a lower possibility, and wherein the numerical value increases with an increase in said bond energy and the value decreases with an increase in the distance between said paired sequences;
- (h) assigning the numerical value obtained in step (g) to each nucleotide of the sequences;
 - (i) repeating the steps (b) through (h) starting with different region from that already selected in step (b), until all allowable second sequences for said first sequence have been selected;
 - (j) repeating steps (a) through (i) for all possible first sequences on the target mRNA or its precursor without selecting the same pair more than once;
 - (k) summing the numerical values, which are assigned in step (h) for all sequences selected in steps (a) through (j), for each nucleotide in the mRNA or its precursor;
 - (l) selecting one or more regions which consist of at least 6 contiguous nucleotides and have a low summed value relative to another region; and
 - (m) designing an antisense oligonucleotide complementary to said region selected in step (l).
19. (New) The method of claim 18, wherein said numerical value is expressed as $((L+1)/r)^F \exp(|\Delta G|/RT)$, wherein ΔG is the bond energy for forming a complementary double-stranded region, R is the gas constant, T is the absolute temperature, L is an integer from 3 to 10, r is one plus the number of nucleic acid bases between said first target region and said complementary region, with the provision that $r > L+1$, and F is a positive number not greater than 6.
20. (New) The method of claim 19, wherein $|\Delta G|$ is determined by the nearest neighbor model.
21. (New) The method of claim 19, wherein L is 4 to 6.

22. (New) The method of claim 19, wherein L is 4.
23. (New) The method of claim 19, wherein F is 6.
24. (New) The method of claim 19, wherein L is 4 to 6, and $|\Delta G|$ is determined by the nearest neighbor model.
25. (New) The method of claim 19, wherein L is 4, and $|\Delta G|$ is determined by the nearest neighbor model.